

## SEQUENCE LISTING

<110> Myriad Genetics, Inc.  
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Bartel, Paul L.

<120> Protein-Protein Interactions

<130> 2318-278-II

<150> US 60/256,986

<151> 2000-12-21

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 40

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide primer

<400> 1

gcaggaaaca gctatgacca tacagtcagc ggccgccacc

40

<210> 2

<211> 39

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide primer

<400> 2

acggccagtc gcgtggagtg ttatgtcatg cgcccgcta

39

<210> 3

<211> 528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(528)

<223> Xaa is Gly or Cys

<400> 3

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Ala Asn Arg Asn Gly Gly Tyr Gly Cys Val Cys Val Asn Gly Trp Ser  
1 5 10 15

48

gga gat gac tgc agt gag aac att gat gat tgt gcc ttc gcc tcc tgt  
Gly Asp Asp Cys Ser Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys  
20 25 30

96

act cca ggc tcc acc tgc atc gac cgt gtg gcc tcc ttc tct tgc atg  
Thr Pro Gly Ser Thr Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met  
35 40 45

144

ttc cca gag ggg aag gca ggt ctc ctg tgt cat ctg gat gat gca tgc  
Phe Pro Glu Gly Lys Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys

192

50	55	60	
atc agc aat cct tgc cac aag ggg gca ttg tgt gac acc aac ccc cta Ile Ser Asn Pro Cys His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu 65 70 75 80			240
aat ggg caa tat att tgc acc tgc cca caa ggc tac aaa ggg gct gac Asn Gly Gln Tyr Ile Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp 85 90 95			288
tgc aca gaa gat gtg gat gaa tgt gcc atg gcc aat agc aat cct tgt Cys Thr Glu Asp Val Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys 100 105 110			336
gag cat gca gga aaa tgt gtg aac acg gat ggc gcc ttc cac tgt gag Glu His Ala Gly Lys Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu 115 120 125			384
tgt ctg aag ggt tat gca gga cct cgt tgt gag atg gac atc aat gag Cys Leu Lys Gly Tyr Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu 130 135 140			432
tgc cat tca gac ccc tgc cag aat gat gct acc tgt ctg gat aag att Cys His Ser Asp Pro Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile 145 150 155 160			480
gga ggc ttc aca tgt ctg tgc cat gcc agg ttt caa agg kgt gca ttg Gly Gly Phe Thr Cys Leu Cys His Ala Arg Phe Gln Arg Xaa Ala Leu 165 170 175			528
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<213> Homo sapiens			
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Gly Asp Asp Cys Ser Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys 20 25 30			
Thr Pro Gly Ser Thr Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met 35 40 45			
Phe Pro Glu Gly Lys Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys 50 55 60			
Ile Ser Asn Pro Cys His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu 65 70 75 80			
Asn Gly Gln Tyr Ile Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp 85 90 95			
Cys Thr Glu Asp Val Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys 100 105 110			
Glu His Ala Gly Lys Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu 115 120 125			

Cys Leu Lys Gly Tyr Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu  
130 135 140

Cys His Ser Asp Pro Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile  
145 150 155 160

Gly Gly Phe Thr Cys Leu Cys His Ala Arg Phe Gln Arg Xaa Ala Leu  
165 170 175

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<213> Homo sapiens

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tgt gtg gcc cag gcc atg ctg gga aaa gcc acg tgc cgg tgt gcc tca 96  
Cys Val Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser  
20 25 30  
ggg ttt aca gga gag gac tgc cag tac tcg aca cct cat cca tgc ttt 144  
Gly Phe Thr Gly Glu Asp Cys Gln Tyr Ser Thr Pro His Pro Cys Phe  
35 40 45  
gtg tct cga cct tgc ctg aat ggc ggc aca tgc cat atg ctc agc cgg 192  
Val Ser Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg  
50 55 60  
gat acc tat gag tgc acc tgt caa gtc ggg ttt aca ggt aag gag tgc 240  
Asp Thr Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys  
65 70 75 80  
caa tgg acc gat gcc tgc ctg tct cat ctc tgt gca aat gga agt acc 288  
Gln Trp Thr Asp Ala Cys Leu Ser His Leu Cys Ala Asn Gly Ser Thr  
85 90 95  
tgt acc act gtg gcc aac cag ttc tcc tgc aaa tgc ctc aca ggc ttc 336  
Cys Thr Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe  
100 105 110  
aca ggg cag aag tgt gag act gat gtc aat gag tgt gac att cca gga 384  
Thr Gly Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly  
115 120 125  
cac tgc cag ctt ggt ggc acc tgc ctc aac ctg cct ggt tcc tac cag 432  
His Cys Gln Leu Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln  
130 135 140  
tgc cag tgc ctt cag ggc ttc aca ggc cag tac tgt gac aga ctg tat 480  
Cys Gln Cys Leu Gln Gly Phe Thr Gly Gln Tyr Cys Asp Arg Leu Tyr  
145 150 155 160  
gtg ccc tgt gca cac tcg cct tgt gtc aat gga ggc tcc tgt cgg cag 528  
Val Pro Cys Ala His Ser Pro Cys Val Asn Gly Gly Ser Cys Arg Gln  
165 170 175

act ggt gac ttc act ttt gag tgc aac tgc ctt cca gag tat gaa gag 576  
 Thr Gly Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Glu Tyr Glu Glu  
 180 185 190

tgt aag gac ctc ata aaa ttt atg ctg agg aat gag cga cag ttc aag 624  
 Cys Lys Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys  
 195 200 205

gag gag ttc ctg ttc tgc agc ttg cac tac 654  
 Glu Glu Phe Leu Phe Ser Ser Leu His Tyr  
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<210> 6  
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 <212> PRT  
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<400> 6  
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 20 25 30

Gly Phe Thr Gly Glu Asp Cys Gln Tyr Ser Thr Pro His Pro Cys Phe  
 35 40 45

Val Ser Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg  
 50 55 60

Asp Thr Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys  
 65 70 75 80

Gln Trp Thr Asp Ala Cys Leu Ser His Leu Cys Ala Asn Gly Ser Thr  
 85 90 95

Cys Thr Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe  
 100 105 110

Thr Gly Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly  
 115 120 125

His Cys Gln Leu Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln  
 130 135 140

Cys Gln Cys Leu Gln Gly Phe Thr Gly Gln Tyr Cys Asp Arg Leu Tyr  
 145 150 155 160

Val Pro Cys Ala His Ser Pro Cys Val Asn Gly Gly Ser Cys Arg Gln  
 165 170 175

Thr Gly Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Glu Tyr Glu Glu  
 180 185 190

Cys Lys Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys  
 195 200 205

Glu Glu Phe Leu Phe Ser Ser Leu His Tyr  
 210 215